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SEQUENCE LISTING

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<120> Transcriptional Activator Nucleic Acids,
Polypeptides, and Methods of Use Thereof

<130> 0943

<140> 09/435,054

<141> 1999-11-08

<150> 60/107,643

<151> 1998-11-09

<160> 23

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1173

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (69)...(902)

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gagagcca atg gac tcc agc agc ttc ctc cct gcc gcc ggc gcg gag aat	110
Met Asp Ser Ser Ser Phe Leu Pro Ala Ala Gly Ala Glu Asn	
1 5 10	
ggc tcg gcg gcg ggc ggc gcc aac aat ggc ggc gct gct cag cag cat	158
Gly Ser Ala Ala Gly Gly Ala Asn Asn Gly Gly Ala Ala Gln Gln His	
15 20 25 30	
gcg gcg ccg gcg atc cgc gag cag gac cgg ctg atg ccg atc gcg aac	206
Ala Ala Pro Ala Ile Arg Glu Gln Asp Arg Leu Met Pro Ile Ala Asn	
35 40 45	
gtg atc cgc atc atg cgg cgc gtg ctg ccg gcg cac gcc aag atc tcg	254
Val Ile Arg Ile Met Arg Arg Val Leu Pro Ala His Ala Lys Ile Ser	
50 55 60	
gac gac gcc aag gag acg atc cag gag tgc gtg tcg gag tac atc agc	302
Asp Asp Ala Lys Glu Thr Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser	
65 70 75	
ttc atc acg ggg gag gcc aac gag cgg tgc cag cgg gag cag cgc aag	350
Phe Ile Thr Gly Glu Ala Asn Glu Arg Cys Gln Arg Glu Gln Arg Lys	

80	85	90	
acc atc acc gcc gag gac gtg ctg tgg gcc atg agc cgc ctc ggc ttc			398
Thr Ile Thr Ala Glu Asp Val Leu Trp Ala Met Ser Arg Leu Gly Phe			
95	100	105 110	
gac gac tac gtc gag ccg ctc ggc gcc tac ctc cac cgc tac cgc gag			446
Asp Asp Tyr Val Glu Pro Leu Gly Ala Tyr Leu His Arg Tyr Arg Glu			
115	120	125	
ttc gag ggc gac gcg cgc ggc gtc ggg ctc gtc ccg ggg gcc gcc cca			494
Phe Glu Gly Asp Ala Arg Gly Val Gly Leu Val Pro Gly Ala Ala Pro			
130	135	140	
tcg cgc ggc ggc gac cac cac ccg cac tcc atg tcg cca gcg gcg atg			542
Ser Arg Gly Gly Asp His His Pro His Ser Met Ser Pro Ala Ala Met			
145	150	155	
ctc aag tcc cgc ggg cca gtc tcc gga gcc gcc atg cta ccg cac cac			590
Leu Lys Ser Arg Gly Pro Val Ser Gly Ala Ala Met Leu Pro His His			
160	165	170	
cac cac cac cac gac atg cag atg cac gcc gcc atg tac ggg gga acg			638
His His His His Asp Met Gln Met His Ala Ala Met Tyr Gly Gly Thr			
175	180	185 190	
gcc gtg ccc ccg ccg gcc ggg cct cct cac cac ggc ggg ttc ctc atg			686
Ala Val Pro Pro Pro Ala Gly Pro Pro His His Gly Gly Phe Leu Met			
195	200	205	
cca cac cca cag ggt agt agc cac tac ctg cct tac gcg tac gag ccc			734
Pro His Pro Gln Gly Ser Ser His Tyr Leu Pro Tyr Ala Tyr Glu Pro			
210	215	220	
acg tac ggc ggt gag cac gcc atg gct gca tac tat gga ggc gcc gcg			782
Thr Tyr Gly Gly Glu His Ala Met Ala Ala Tyr Tyr Gly Gly Ala Ala			
225	230	235	
tac gcg ccc ggc aac ggc ggg agc ggc gac ggc agt ggc agt ggc ggc			830
Tyr Ala Pro Gly Asn Gly Gly Ser Gly Asp Gly Ser Gly Ser Gly Gly			
240	245	250	
ggt ggc ggg agc gcg tcg cac aca ccg cag ggc agc ggc ggc ttg gag			878
Gly Gly Gly Ser Ala Ser His Thr Pro Gln Gly Ser Gly Gly Leu Glu			
255	260	265 270	
cac ccg cac ccg ttc gcg tac aag tagctagttc gtacgtcgtt cgacttgagc			932
His Pro His Pro Phe Ala Tyr Lys			
275			
aagccatcga tctgctgacg tgaacgtacg ctgtattgta cacgcatgca cgtacgtatc			992
ggcggttagc tctcctgttt aagttgtact gtgattctgt ccggccggc tagcaactta			1052
gtatcttccct tcagttctta gtttcttagc agtcgtagaa gtgttcaatg cttgccagtg			1112
tggtgtttta gggccggggg aaaccatccg atgagattat ttcaaaaaaa aaaaaaaaaa			1172
a			1173

<210> 2
 <211> 278
 <212> PRT
 <213> Zea mays

<400> 2

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 1 5 10 15
 Ala Ala Gly Gly Ala Asn Asn Gly Gly Ala Ala Gln Gln His Ala Ala
 20 25 30
 Pro Ala Ile Arg Glu Gln Asp Arg Leu Met Pro Ile Ala Asn Val Ile
 35 40 45
 Arg Ile Met Arg Arg Val Leu Pro Ala His Ala Lys Ile Ser Asp Asp
 50 55 60
 Ala Lys Glu Thr Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser Phe Ile
 65 70 75 80
 Thr Gly Glu Ala Asn Glu Arg Cys Gln Arg Glu Gln Arg Lys Thr Ile
 85 90 95
 Thr Ala Glu Asp Val Leu Trp Ala Met Ser Arg Leu Gly Phe Asp Asp
 100 105 110
 Tyr Val Glu Pro Leu Gly Ala Tyr Leu His Arg Tyr Arg Glu Phe Glu
 115 120 125
 Gly Asp Ala Arg Gly Val Gly Leu Val Pro Gly Ala Ala Pro Ser Arg
 130 135 140
 Gly Gly Asp His His Pro His Ser Met Ser Pro Ala Ala Met Leu Lys
 145 150 155 160
 Ser Arg Gly Pro Val Ser Gly Ala Ala Met Leu Pro His His His His
 165 170 175
 His His Asp Met Gln Met His Ala Ala Met Tyr Gly Gly Thr Ala Val
 180 185 190
 Pro Pro Pro Ala Gly Pro Pro His His Gly Gly Phe Leu Met Pro His
 195 200 205
 Pro Gln Gly Ser Ser His Tyr Leu Pro Tyr Ala Tyr Glu Pro Thr Tyr
 210 215 220
 Gly Gly Glu His Ala Met Ala Ala Tyr Tyr Gly Gly Ala Ala Tyr Ala
 225 230 235 240
 Pro Gly Asn Gly Gly Ser Gly Asp Gly Ser Gly Ser Gly Gly Gly Gly
 245 250 255
 Gly Ser Ala Ser His Thr Pro Gln Gly Ser Gly Gly Leu Glu His Pro
 260 265 270
 His Pro Phe Ala Tyr Lys
 275

<210> 3
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 3
 tagtagcgag agccaatgga
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<210> 4
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 4
 gccgggacag aatcacagta
 20

<210> 5

<211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 5
 tagtagcgag agccaatgga
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<210> 6
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 6
 cccggcccta aaacaacaca
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<210> 7
 <211> 481
 <212> DNA
 <213> Argemone mexicana

<220>
 <221> CDS
 <222> (44)...(481)

<221> misc_feature
 <222> (1)...(481)
 <223> n = A,T,C or G

<400> 7
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 ggt ggt ggt ggt ggt agt ggt ggt ggt ttc cat gga tat cag aaa ctc 103
 Gly Gly Gly Gly Gly Ser Gly Gly Gly Phe His Gly Tyr Gln Lys Leu
 5 10 15 20
 cca aaa tca aac tcc gct gga atg atg ctc tcg gag cta tcg aat aac 151
 Pro Lys Ser Asn Ser Ala Gly Met Met Leu Ser Glu Leu Ser Asn Asn
 25 30 35
 aac aac aat att gac gta aac tct aca tgt act gta cga gag caa gat 199
 Asn Asn Asn Ile Asp Val Asn Ser Thr Cys Thr Val Arg Glu Gln Asp
 40 45 50
 cga tac atg cca att gct aat gtg atc agg atc atg cgt aag gta ctt 247
 Arg Tyr Met Pro Ile Ala Asn Val Ile Arg Ile Met Arg Lys Val Leu
 55 60 65
 cct act cat gcc aag atc tct gac gat gcc aaa gaa act atc caa gaa 295
 Pro Thr His Ala Lys Ile Ser Asp Asp Ala Lys Glu Thr Ile Gln Glu
 70 75 80
 tgt gtc tca gaa tac atc agt ttc atc aca agt gaa gcc aat gat cgt 343

Cys Val Ser Glu Tyr Ile Ser Phe Ile Thr Ser Glu Ala Asn Asp Arg
 85 90 95 100

tgc caa cgt gaa caa aga aag aca atc aca gct gaa gat gtt tta tgg 391
 Cys Gln Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu Asp Val Leu Trp
 105 110 115

gcg atg agc aaa cta ggg ntt gat gag tac att gaa cct cta act ctt 439
 Ala Met Ser Lys Leu Gly Xaa Asp Glu Tyr Ile Glu Pro Leu Thr Leu
 120 125 130

tac ctt caa cgt tat cgt gag ttt gaa ggt gna cgt tgg tca 481
 Tyr Leu Gln Arg Tyr Arg Glu Phe Glu Gly Xaa Arg Trp Ser
 135 140 145

<210> 8
 <211> 146
 <212> PRT
 <213> Argemone mexicana

<220>
 <221> VARIANT
 <222> (1)...(146)
 <223> Xaa = Any Amino Acid

<400> 8

Met Glu Arg Gly Gly Gly Gly Gly Ser Gly Gly Gly Phe His Gly
 1 5 10 15
 Tyr Gln Lys Leu Pro Lys Ser Asn Ser Ala Gly Met Met Leu Ser Glu
 20 25 30
 Leu Ser Asn Asn Asn Asn Ile Asp Val Asn Ser Thr Cys Thr Val
 35 40 45
 Arg Glu Gln Asp Arg Tyr Met Pro Ile Ala Asn Val Ile Arg Ile Met
 50 55 60
 Arg Lys Val Leu Pro Thr His Ala Lys Ile Ser Asp Asp Ala Lys Glu
 65 70 75 80
 Thr Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser Phe Ile Thr Ser Glu
 85 90 95
 Ala Asn Asp Arg Cys Gln Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu
 100 105 110
 Asp Val Leu Trp Ala Met Ser Lys Leu Gly Xaa Asp Glu Tyr Ile Glu
 115 120 125
 Pro Leu Thr Leu Tyr Leu Gln Arg Tyr Arg Glu Phe Glu Gly Xaa Arg
 130 135 140
 Trp Ser
 145

<210> 9
 <211> 942
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (3)...(722)

<400> 9

gc acg agc tct ctt ata atc aca cac aca cct acc tta ata gct atg 47
 Thr Ser Ser Leu Ile Thr His Thr Pro Thr Leu Ile Ala Met
 1 5 10 15

gaa act gga ggc ttt cac ggc tac cgc aag ctc ccc aac acc acc gct Glu Thr Gly Gly Phe His Gly Tyr Arg Lys Leu Pro Asn Thr Thr Ala	95
20 25 30	
ggg ttg aag ctg tca gtg tca gac atg aac atg agg cag cag gta gca Gly Leu Lys Leu Ser Val Ser Asp Met Asn Met Arg Gln Gln Val Ala	143
35 40 45	
tca tca gat cac agt gca gcc aca gga gag gag aac gaa tgc acg gtg Ser Ser Asp His Ser Ala Ala Thr Gly Glu Glu Asn Glu Cys Thr Val	191
50 55 60	
agg gag caa gac agg ttc atg cca atc gcc aac gtg att agg atc atg Arg Glu Gln Asp Arg Phe Met Pro Ile Ala Asn Val Ile Arg Ile Met	239
65 70 75	
cgc aag att ctc cct cca cac gca aaa atc tcg gac gat gca aaa gaa Arg Lys Ile Leu Pro Pro His Ala Lys Ile Ser Asp Asp Ala Lys Glu	287
80 85 90 95	
aca atc caa gag tgc gtg tct gag tac atc agc ttc atc aca ggt gag Thr Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser Phe Ile Thr Gly Glu	335
100 105 110	
gcg aac gag cgt tgc cag agg gag cag cgg aag acc ata acc gca gag Ala Asn Glu Arg Cys Gln Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu	383
115 120 125	
gac gtg ctt tgg gcc atg agc aag ctt gga ttc gac gac tac atc gaa Asp Val Leu Trp Ala Met Ser Lys Leu Gly Phe Asp Asp Tyr Ile Glu	431
130 135 140	
ccg ttg acc atg tac ctt cac cgc tac cgt gaa ctt gag ggt gac cgc Pro Leu Thr Met Tyr Leu His Arg Tyr Arg Glu Leu Glu Gly Asp Arg	479
145 150 155	
acc tct atg agg ggt gaa cca ctc ggg aag agg act gtg gaa tac gcc Thr Ser Met Arg Gly Glu Pro Leu Gly Lys Arg Thr Val Glu Tyr Ala	527
160 165 170 175	
acg ctt ggt gtt gct act gct ttt gtc cct cca ccc tat cat cac cac Thr Leu Gly Val Ala Thr Ala Phe Val Pro Pro Pro Tyr His His His	575
180 185 190	
aat ggg tac ttt ggt gct gcc atg ccc atg ggg act tac gtt agg gaa Asn Gly Tyr Phe Gly Ala Ala Met Pro Met Gly Thr Tyr Val Arg Glu	623
195 200 205	
gcg cca cca aat aca gcc tcc tcc cat cac cac cac cac cac cac Ala Pro Pro Asn Thr Ala Ser Ser His His His His His His His	671
210 215 220	
cac cat gct cgt gga atc tcc aat gct cat gaa cca aat gct cgc tcc His His Ala Arg Gly Ile Ser Asn Ala His Glu Pro Asn Ala Arg Ser	719
225 230 235	
ata taaaattata taattatgac taggattcag aacaagactt gatgatgatt Ile	772
240	
agcttaactc tcagtaattg gtgctagagt actactgttg ttgaggatac tttattttat aattaagggc tgggaaggga gttagtatat tcctaactct aactatgtgc atctttaatt	832 892

tatgaaatca ctttgtttta acctttgatg aaaaaaaaaa aaaaaaaaaa

942

<210> 10
 <211> 240
 <212> PRT
 <213> Glycine max

<400> 10
 Thr Ser Ser Leu Ile Ile Thr His Thr Pro Thr Leu Ile Ala Met Glu
 1 5 10 15
 Thr Gly Gly Phe His Gly Tyr Arg Lys Leu Pro Asn Thr Thr Ala Gly
 20 25 30
 Leu Lys Leu Ser Val Ser Asp Met Asn Met Arg Gln Gln Val Ala Ser
 35 40 45
 Ser Asp His Ser Ala Ala Thr Gly Glu Glu Asn Glu Cys Thr Val Arg
 50 55 60
 Glu Gln Asp Arg Phe Met Pro Ile Ala Asn Val Ile Arg Ile Met Arg
 65 70 75 80
 Lys Ile Leu Pro Pro His Ala Lys Ile Ser Asp Asp Ala Lys Glu Thr
 85 90 95
 Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser Phe Ile Thr Gly Glu Ala
 100 105 110
 Asn Glu Arg Cys Gln Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu Asp
 115 120 125
 Val Leu Trp Ala Met Ser Lys Leu Gly Phe Asp Asp Tyr Ile Glu Pro
 130 135 140
 Leu Thr Met Tyr Leu His Arg Tyr Arg Glu Leu Glu Gly Asp Arg Thr
 145 150 155 160
 Ser Met Arg Gly Glu Pro Leu Gly Lys Arg Thr Val Glu Tyr Ala Thr
 165 170 175
 Leu Gly Val Ala Thr Ala Phe Val Pro Pro Pro Tyr His His Asn
 180 185 190
 Gly Tyr Phe Gly Ala Ala Met Pro Met Gly Thr Tyr Val Arg Glu Ala
 195 200 205
 Pro Pro Asn Thr Ala Ser Ser His His His His His His His
 210 215 220
 His Ala Arg Gly Ile Ser Asn Ala His Glu Pro Asn Ala Arg Ser Ile
 225 230 235 240

<210> 11
 <211> 905
 <212> DNA
 <213> Veronia mespilifolia

<220>
 <221> CDS
 <222> (58)...(699)

<400> 11
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 60

Met
 1

gaa cgt gga gga ggt ttc cat ggc tac cac agg ctc ccc atc cac cct
 Glu Arg Gly Gly Gly Phe His Gly Tyr His Arg Leu Pro Ile His Pro 108
 5 10 15

aca tct gga atc caa caa tcg gat atg aag cta aag cta cca gaa atg
 Thr Ser Gly Ile Gln Gln Ser Asp Met Lys Leu Lys Leu Pro Glu Met 156
 20 25 30

acc aac aat aac tcg tcc act gat gac aat gag tgc acc gtt cga gaa 204
 Thr Asn Asn Asn Ser Ser Thr Asp Asp Asn Glu Cys Thr Val Arg Glu
 35 40 45
 cag gac cgc ttc atg ccg ata gca aac gtg atc cgc atc atg cgg aag 252
 Gln Asp Arg Phe Met Pro Ile Ala Asn Val Ile Arg Ile Met Arg Lys
 50 55 60 65
 atc ctt cct cca cat gcc aag atc tct gat gat gcc aaa gag acg atc 300
 Ile Leu Pro Pro His Ala Lys Ile Ser Asp Asp Ala Lys Glu Thr Ile
 70 75 80
 caa gaa tgt gtt tca gag tac att agc ttt gtc aca ggc gag gca aat 348
 Gln Glu Cys Val Ser Glu Tyr Ile Ser Phe Val Thr Gly Glu Ala Asn
 85 90 95
 gac cgc tgc cag cgt gag caa agg aag acc atc aca gct gaa gat gtg 396
 Asp Arg Cys Gln Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu Asp Val
 100 105 110
 ctc tgg gct atg agc aaa ctg gga ttt gat gat tat atc gag ccc ttg 444
 Leu Trp Ala Met Ser Lys Leu Gly Phe Asp Asp Tyr Ile Glu Pro Leu
 115 120 125
 act gtg tat ctc cat cgc tac agg gag ttt gat ggt ggc gaa cgt gga 492
 Thr Val Tyr Leu His Arg Tyr Arg Glu Phe Asp Gly Gly Glu Arg Gly
 130 135 140 145
 tcc ata agg ggt gag ccc ctt gtg aag agg agt act tct gat cct ggt 540
 Ser Ile Arg Gly Glu Pro Leu Val Lys Arg Ser Thr Ser Asp Pro Gly
 150 155 160
 cac ttt ggg atg gct tct ttt gtg cct gct ttt cat atg ggt cat cat 588
 His Phe Gly Met Ala Ser Phe Val Pro Ala Phe His Met Gly His His
 165 170 175
 aac ggc ttc ttt ggt cct gca agc att ggt ggt ttc ctg aaa gac cca 636
 Asn Gly Phe Phe Gly Pro Ala Ser Ile Gly Gly Phe Leu Lys Asp Pro
 180 185 190
 tcg agt gct ggc cct tcg gga cct gca gtc gct ggg ttt gag ccg tat 684
 Ser Ser Ala Gly Pro Ser Gly Pro Ala Val Ala Gly Phe Glu Pro Tyr
 195 200 205
 gct cag tgt aaa gag taactgcaaa aagtaggggt tgggatgaga tgatgatgat 739
 Ala Gln Cys Lys Glu
 210
 ggtggtggtg gtggtggttt gttttgtttt gttctttctt ttttttttct tctttctttt 799
 cttggtcatt gaggaacaaa cttacattgg ttcactttgg ctaggcatgt aaacggttaa 859
 catgcttatc aagtagtagt tttcgatcaa aaaaaaaaaa aaaaaa 905
 <210> 12
 <211> 214
 <212> PRT
 <213> *Veronia mespilifolia*
 <400> 12
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 1 5 10 15
 Pro Thr Ser Gly Ile Gln Gln Ser Asp Met Lys Leu Lys Leu Pro Glu
 20 25 30

Met Thr Asn Asn Asn Ser Ser Thr Asp Asp Asn Glu Cys Thr Val Arg
 35 40 45
 Glu Gln Asp Arg Phe Met Pro Ile Ala Asn Val Ile Arg Ile Met Arg
 50 55 60
 Lys Ile Leu Pro Pro His Ala Lys Ile Ser Asp Ala Lys Glu Thr
 65 70 75 80
 Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser Phe Val Thr Gly Glu Ala
 85 90 95
 Asn Asp Arg Cys Gln Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu Asp
 100 105 110
 Val Leu Trp Ala Met Ser Lys Leu Gly Phe Asp Asp Tyr Ile Glu Pro
 115 120 125
 Leu Thr Val Tyr Leu His Arg Tyr Arg Glu Phe Asp Gly Gly Glu Arg
 130 135 140
 Gly Ser Ile Arg Gly Glu Pro Leu Val Lys Arg Ser Thr Ser Asp Pro
 145 150 155 160
 Gly His Phe Gly Met Ala Ser Phe Val Pro Ala Phe His Met Gly His
 165 170 175
 His Asn Gly Phe Phe Gly Pro Ala Ser Ile Gly Gly Phe Leu Lys Asp
 180 185 190
 Pro Ser Ser Ala Gly Pro Ser Gly Pro Ala Val Ala Gly Phe Glu Pro
 195 200 205
 Tyr Ala Gln Cys Lys Glu
 210

<210> 13
 <211> 763
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (1)...(480)

<400> 13

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cgc ctc ggc ttc gac gac tac gtc gcg ccc ctc ggc gcc ttc ctc cag Arg Leu Gly Phe Asp Asp Tyr Val Ala Pro Leu Gly Ala Phe Leu Gln 20 25 30	96
cgc atg cgc gac gac agc gac cac ggc ggt gaa gag cgc ggc ggc cct Arg Met Arg Asp Asp Ser Asp His Gly Gly Glu Glu Arg Gly Gly Pro 35 40 45	144
gca ggg cgt ggt ggc tcg cgc cgc ggc tcg tcg tcc ttg ccg ctc cac Ala Gly Arg Gly Gly Ser Arg Arg Gly Ser Ser Ser Leu Pro Leu His 50 55 60	192
tgc ccg cag cag atg cac cac ctg cac cca gcc gtc tgc cgg cgt ccg Cys Pro Gln Gln Met His His Leu His Pro Ala Val Cys Arg Arg Pro 65 70 75 80	240
cac cag agc gtg tcg cct gct gca gga tac gcc gtc cgg ccc gtt ccc His Gln Ser Val Ser Pro Ala Ala Gly Tyr Ala Val Arg Pro Val Pro 85 90 95	288
cgc ccg atg cca gcc cgt ggg tac cgc atg cag ggc gga gac cac cgc Arg Pro Met Pro Ala Arg Gly Tyr Arg Met Gln Gly Gly Asp His Arg 100 105 110	336

agc gtg ggc ggc gtg gct ccc tgc agc tac gga ggg gcg ctc gtc cag 384
 Ser Val Gly Gly Val Ala Pro Cys Ser Tyr Gly Gly Ala Leu Val Gln
 115 120 125

gcc ggt gga acc caa cac gtt gtt gga ttc cac gac gac gag gca agc 432
 Ala Gly Gly Thr Gln His Val Val Gly Phe His Asp Asp Glu Ala Ser
 130 135 140

tct tcg agt gaa aat ccg ccg ccg gag ggg cgt gcc gct ggc tcg aac 480
 Ser Ser Ser Glu Asn Pro Pro Pro Glu Gly Arg Ala Ala Gly Ser Asn
 145 150 155 160

tagcctagct tctcagttcc ccgtgtacaa taagaggggc ggtagcgccg ccgagccgag 540
 cccttgggtt gggccgggag ctatgctgca gtttggtttg taaactaacg agcctagggt 600
 agctgggtgca cgcgcgccac ctgcccggac gtcgccgtcg tcgtcgcat ggacttaacc 660
 ggcgggccct gttgttattt ctcaagtttg tagccaacgc actgttcggt gcgttcata 720
 atttaattta ccattgttgct ctcgaaaaaa aaaaaaaaaa aaa 763

<210> 14
 <211> 160
 <212> PRT
 <213> Zea mays

<400> 14
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 1 5 10 15
 Arg Leu Gly Phe Asp Asp Tyr Val Ala Pro Leu Gly Ala Phe Leu Gln
 20 25 30
 Arg Met Arg Asp Asp Ser Asp His Gly Gly Glu Glu Arg Gly Gly Pro
 35 40 45
 Ala Gly Arg Gly Gly Ser Arg Arg Gly Ser Ser Ser Leu Pro Leu His
 50 55 60
 Cys Pro Gln Gln Met His His Leu His Pro Ala Val Cys Arg Arg Pro
 65 70 75 80
 His Gln Ser Val Ser Pro Ala Ala Gly Tyr Ala Val Arg Pro Val Pro
 85 90 95
 Arg Pro Met Pro Ala Arg Gly Tyr Arg Met Gln Gly Gly Asp His Arg
 100 105 110
 Ser Val Gly Gly Val Ala Pro Cys Ser Tyr Gly Gly Ala Leu Val Gln
 115 120 125
 Ala Gly Gly Thr Gln His Val Val Gly Phe His Asp Asp Glu Ala Ser
 130 135 140
 Ser Ser Ser Glu Asn Pro Pro Pro Glu Gly Arg Ala Ala Gly Ser Asn
 145 150 155 160

<210> 15
 <211> 622
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (3)...(622)
 <221> misc_feature
 <222> (1)...(622)
 <223> n = A,T,C or G

<400> 15
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 Met Asn Asn Pro Gln Asn Pro Lys Ala Ser Ala Pro Cys Thr Leu

1	5	10	15	
cca ccg gag ctt ccc	aaa gaa gca gtg	gcg acc gac gaa gca ccg ccg		95
Pro Pro Glu Leu Pro	Lys Glu Ala Val	Ala Thr Asp Glu Ala Pro Pro		
	20	25	30	
cca atg ggc aac aac aac aac acg	gaa tcg gcg acg gcg acg atg gtc		143	
Pro Met Gly Asn Asn Asn Thr	Glu Ser Ala Thr Ala Thr Met Val			
	35	40	45	
cgg gag cag gac cgg ctg atg ccc	gtg gcc aac gtg tcc cgc atc atg		191	
Arg Glu Gln Asp Arg Leu Met Pro	Val Ala Asn Val Ser Arg Ile Met			
	50	55	60	
cgc caa gtg ctg cct ccg tac gcc	aag atc tcc gac gac gcc can gaa		239	
Arg Gln Val Leu Pro Pro Tyr	Ala Lys Ile Ser Asp Asp Ala Xaa Glu			
	65	70	75	
gtn atc caa gaa ttg ctn ttc gga	att tca tca ctt ncg tcc tgg cga		287	
Xaa Ile Gln Glu Leu Xaa Phe Gly	Ile Ser Ser Leu Xaa Ser Trp Arg			
	80	85	90	95
ggc gaa acg aag cgg tgc cac acc	gag cgc cgc aag acc gtc acc tcc		335	
Gly Glu Thr Lys Arg Cys His Thr	Glu Arg Arg Lys Thr Val Thr Ser			
	100	105	110	
gaa gac atc gtg tgg gcc atg agc	cgc ctc ggc ttc gac gac tac gtc		383	
Glu Asp Ile Val Trp Ala Met Ser	Arg Leu Gly Phe Asp Asp Tyr Val			
	115	120	125	
gcg ccc ctc ggc gcc ttc ctc cag	cgc atg cgc gac nac agc gaa cac		431	
Ala Pro Leu Gly Ala Phe Leu Gln	Arg Met Arg Asp Xaa Ser Glu His			
	130	135	140	
ggg ggt gaa aac gcg gcg gcc tgc	ang ggg tng tgg tcn cgc cgc ggg		479	
Gly Gly Glu Asn Ala Ala Ala Cys	Xaa Gly Xaa Trp Xaa Arg Arg Gly			
	145	150	155	
tcg tct nct tgg cgc tcc ctt gcc	gca ana gat gac aac ttg cac caa		527	
Ser Ser Xaa Trp Arg Ser Leu Ala	Ala Xaa Asp Asp Asn Leu His Gln			
	160	165	170	175
acg tct gcc ggg ntc gga cca aaa	ctn ttc cct gtt gca gga ata ccc		575	
Thr Ser Ala Gly Xaa Gly Pro Lys	Xaa Phe Pro Val Ala Gly Ile Pro			
	180	185	190	
gtc cng ggc cnt tcc ccc ccn aat	cca acc att tgg ttt ccc ctt gc		622	
Val Xaa Gly Xaa Ser Pro Xaa Asn	Pro Thr Ile Trp Phe Pro Leu			
	195	200	205	

<210> 16
 <211> 206
 <212> PRT
 <213> Zea mays

<220>
 <221> VARIANT
 <222> (1)...(206)
 <223> Xaa = Any Amino Acid

<400> 16

Met Asn Asn Pro Gln Asn Pro Lys Ala Ser Ala Pro Cys Thr Leu Pro
 1 5 10 15
 Pro Glu Leu Pro Lys Glu Ala Val Ala Thr Asp Glu Ala Pro Pro Pro
 20 25 30
 Met Gly Asn Asn Asn Thr Glu Ser Ala Thr Ala Thr Met Val Arg
 35 40 45
 Glu Gln Asp Arg Leu Met Pro Val Ala Asn Val Ser Arg Ile Met Arg
 50 55 60
 Gln Val Leu Pro Pro Tyr Ala Lys Ile Ser Asp Ala Xaa Glu Xaa
 65 70 75 80
 Ile Gln Glu Leu Xaa Phe Gly Ile Ser Ser Leu Xaa Ser Trp Arg Gly
 85 90 95
 Glu Thr Lys Arg Cys His Thr Glu Arg Arg Lys Thr Val Thr Ser Glu
 100 105 110
 Asp Ile Val Trp Ala Met Ser Arg Leu Gly Phe Asp Asp Tyr Val Ala
 115 120 125
 Pro Leu Gly Ala Phe Leu Gln Arg Met Arg Asp Xaa Ser Glu His Gly
 130 135 140
 Gly Glu Asn Ala Ala Ala Cys Xaa Gly Xaa Trp Xaa Arg Arg Gly Ser
 145 150 155 160
 Ser Xaa Trp Arg Ser Leu Ala Ala Xaa Asp Asp Asn Leu His Gln Thr
 165 170 175
 Ser Ala Gly Xaa Gly Pro Lys Xaa Phe Pro Val Ala Gly Ile Pro Val
 180 185 190
 Xaa Gly Xaa Ser Pro Xaa Asn Pro Thr Ile Trp Phe Pro Leu
 195 200 205

<210> 17
 <211> 1121
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (3)...(1121)

<400> 17

gc acg agg gaa act gga ggc ttt cat ggc tac cgc aag ctc ccc aac 47
 Thr Arg Glu Thr Gly Gly Phe His Gly Tyr Arg Lys Leu Pro Asn
 1 5 10 15
 aca acc tct ggg ttg aag ctg tca gtg tca gac atg aac atg aac atg 95
 Thr Thr Ser Gly Leu Lys Leu Ser Val Ser Asp Met Asn Met Asn Met
 20 25 30
 agg cag cag cag gta gca tca tca gat cag aac tgc agc aac cac agt 143
 Arg Gln Gln Gln Val Ala Ser Ser Asp Gln Asn Cys Ser Asn His Ser
 35 40 45
 gca gca gga gag gag aac gaa tgc acg gtg agg gag caa gac agg ttc 191
 Ala Ala Gly Glu Glu Asn Glu Cys Thr Val Arg Glu Gln Asp Arg Phe
 50 55 60
 atg cca atc gct aac gtg ata cgg atc atg cgc aag att ctc cct cca 239
 Met Pro Ile Ala Asn Val Ile Arg Ile Met Arg Lys Ile Leu Pro Pro
 65 70 75
 cac gca aaa atc tcc gat gat gca aag gag aca atc caa gag tgc gtg 287
 His Ala Lys Ile Ser Asp Asp Ala Lys Glu Thr Ile Gln Glu Cys Val
 80 85 90 95
 tcg gag tac atc agc ttc atc acc ggg gag gcc aac gag cgt tgc cag 335

Ser Glu Tyr Ile Ser Phe Ile Thr Gly Glu Ala Asn Glu Arg Cys Gln	
100 105 110	
agg gag cag cgc aag acc ata acc gca gag gac gtg ctt tgg gca atg	383
Arg Glu Gln Arg Lys Thr Ile Thr Ala Glu Asp Val Leu Trp Ala Met	
115 120 125	
agt aag ctt gga ttc gac gac tac atc gaa ccg tta acc atg tac ctt	431
Ser Lys Leu Gly Phe Asp Asp Tyr Ile Glu Pro Leu Thr Met Tyr Leu	
130 135 140	
cac cgc tac cgt gag ctg gag ggt gac cgc acc tct atg agg ggt gaa	479
His Arg Tyr Arg Glu Leu Glu Gly Asp Arg Thr Ser Met Arg Gly Glu	
145 150 155	
ccg ctc ggg aag agg act gtg gaa tat gcc acg ctt gct act gct ttt	527
Pro Leu Gly Lys Arg Thr Val Glu Tyr Ala Thr Leu Ala Thr Ala Phe	
160 165 170 175	
gtg ccg cca ccc ttt cat cac cac aat ggc tac ttt ggt gct gcc atg	575
Val Pro Pro Pro Phe His His His Asn Gly Tyr Phe Gly Ala Ala Met	
180 185 190	
ccc atg ggg act tac gtt agg gaa acg cca cca aat gct gcg tca tct	623
Pro Met Gly Thr Tyr Val Arg Glu Thr Pro Pro Asn Ala Ala Ser Ser	
195 200 205	
cat cac cat cat gga atc tcc aat gct cat gaa cca aat gct cgc tcc	671
His His His His Gly Ile Ser Asn Ala His Glu Pro Asn Ala Arg Ser	
210 215 220	
ata taa aat taa tga aga gta ctg ttc agt agg aga aca aga ctt ctt	719
Ile * Asn * * Arg Val Leu Phe Ser Arg Arg Thr Arg Leu Leu	
225 230 235	
gga ctt gat tag ctt aac tct cag tga ttg gtg tta gag tac tgt tgt	767
Gly Leu Asp * Leu Asn Ser Gln * Leu Val Leu Glu Tyr Cys Cys	
240 245 250	
tga gga tgg tta att tta taa tta agg gct ggg aat tgg gga gtt agt	815
* Gly Trp Leu Ile Leu * Leu Arg Ala Gly Asn Trp Gly Val Ser	
255 260	
ata tat tcc taa tcc taa tta tgt gca tct tta att tat gga ata act	863
Ile Tyr Ser * Ser * Leu Cys Ala Ser Leu Ile Tyr Gly Ile Thr	
265 270 275	
ttg ttt ttt gtt tta act tct gat aat ttg gat ttt ctg atg ttt aat	911
Leu Phe Phe Val Leu Thr Ser Asp Asn Leu Asp Phe Leu Met Phe Asn	
280 285 290	
gtg gtt ttg tct atc cct tat taa cag tgc caa gct taa ggt ttt agc	959
Val Val Leu Ser Ile Pro Tyr * Gln Cys Gln Ala * Gly Phe Ser	
295 300 305	
cat gct cca aaa tgg aat act tgt act gtt atg ttg ttc tgg tag tga	1007
His Ala Pro Lys Trp Asn Thr Cys Thr Val Met Leu Phe Trp * *	
310 315 320	
tgg tga tga aac ctg caa gtt atg ttt atg tat aaa gcc act att gat	1055
Trp * * Asn Leu Gln Val Met Phe Met Tyr Lys Ala Thr Ile Asp	
325 330 335	

caa aat tag aga aat tat cat tta ata agt atc ctc cca tgt taa ttt 1103
 Gln Asn * Arg Asn Tyr His Leu Ile Ser Ile Leu Pro Cys * Phe
 340 345 350

taa aaa aaa aaa aaa aaa 1121
 * Lys Lys Lys Lys Lys
 355

<210> 18
 <211> 355
 <212> PRT
 <213> Glycine max

<400> 18
 Thr Arg Glu Thr Gly Gly Phe His Gly Tyr Arg Lys Leu Pro Asn Thr
 1 5 10 15
 Thr Ser Gly Leu Lys Leu Ser Val Ser Asp Met Asn Met Asn Met Arg
 20 25 30
 Gln Gln Gln Val Ala Ser Ser Asp Gln Asn Cys Ser Asn His Ser Ala
 35 40 45
 Ala Gly Glu Glu Asn Glu Cys Thr Val Arg Glu Gln Asp Arg Phe Met
 50 55 60
 Pro Ile Ala Asn Val Ile Arg Ile Met Arg Lys Ile Leu Pro Pro His
 65 70 75 80
 Ala Lys Ile Ser Asp Asp Ala Lys Glu Thr Ile Gln Glu Cys Val Ser
 85 90 95
 Glu Tyr Ile Ser Phe Ile Thr Gly Glu Ala Asn Glu Arg Cys Gln Arg
 100 105 110
 Glu Gln Arg Lys Thr Ile Thr Ala Glu Asp Val Leu Trp Ala Met Ser
 115 120 125
 Lys Leu Gly Phe Asp Asp Tyr Ile Glu Pro Leu Thr Met Tyr Leu His
 130 135 140
 Arg Tyr Arg Glu Leu Glu Gly Asp Arg Thr Ser Met Arg Gly Glu Pro
 145 150 155 160
 Leu Gly Lys Arg Thr Val Glu Tyr Ala Thr Leu Ala Thr Ala Phe Val
 165 170 175
 Pro Pro Pro Phe His His His Asn Gly Tyr Phe Gly Ala Ala Met Pro
 180 185 190
 Met Gly Thr Tyr Val Arg Glu Thr Pro Pro Asn Ala Ala Ser Ser His
 195 200 205
 His His His Gly Ile Ser Asn Ala His Glu Pro Asn Ala Arg Ser Ile
 210 215 220
 Asn Arg Val Leu Phe Ser Arg Arg Thr Arg Leu Leu Gly Leu Asp Leu
 225 230 235 240
 Asn Ser Gln Leu Val Leu Glu Tyr Cys Cys Gly Trp Leu Ile Leu Leu
 245 250 255
 Arg Ala Gly Asn Trp Gly Val Ser Ile Tyr Ser Ser Leu Cys Ala Ser
 260 265 270
 Leu Ile Tyr Gly Ile Thr Leu Phe Phe Val Leu Thr Ser Asp Asn Leu
 275 280 285
 Asp Phe Leu Met Phe Asn Val Val Leu Ser Ile Pro Tyr Gln Cys Gln
 290 295 300
 Ala Gly Phe Ser His Ala Pro Lys Trp Asn Thr Cys Thr Val Met Leu
 305 310 315 320
 Phe Trp Trp Asn Leu Gln Val Met Phe Met Tyr Lys Ala Thr Ile Asp
 325 330 335
 Gln Asn Arg Asn Tyr His Leu Ile Ser Ile Leu Pro Cys Phe Lys Lys
 340 345 350
 Lys Lys Lys
 355

<210> 19
 <211> 796
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (1)... (513)

<400> 19
 gca cga gca atg gcg gga gtg agg gaa cag gac cag tac atg ccg ata 48
 Ala Arg Ala Met Ala Gly Val Arg Glu Gln Asp Gln Tyr Met Pro Ile
 1 5 10 15
 gcg aac gtg ata agg atc atg cgt cgg att ctg cca gcg cac gcg aag 96
 Ala Asn Val Ile Arg Ile Met Arg Arg Ile Leu Pro Ala His Ala Lys
 20 25 30
 atc tca gac gac gcg aag gag acg atc cag gag tgc gtg tct gag tac 144
 Ile Ser Asp Asp Ala Lys Glu Thr Ile Gln Glu Cys Val Ser Glu Tyr
 35 40 45
 atc agt ttc atc acg gcg gag gcg aac gag cgg tgc cag cgg gag cag 192
 Ile Ser Phe Ile Thr Ala Glu Ala Asn Glu Arg Cys Gln Arg Glu Gln
 50 55 60
 cgg aag acg gtg acc gca gag gat gtg ttg tgg gcg atg gag aag ctt 240
 Arg Lys Thr Val Thr Ala Glu Asp Val Leu Trp Ala Met Glu Lys Leu
 65 70 75 80
 ggc ttt gac aac tac gct cac cct ctc tct ctt tac ctt cac cgc tac 288
 Gly Phe Asp Asn Tyr Ala His Pro Leu Ser Leu Tyr Leu His Arg Tyr
 85 90 95
 cgc gag agt gaa gga gaa cct gct tct gtc aga cgc gct tct tct gca 336
 Arg Glu Ser Glu Gly Glu Pro Ala Ser Val Arg Arg Ala Ser Ser Ala
 100 105 110
 atg ggg atc aat aat aat atg gtg cac cca cct tat att aat tct cat 384
 Met Gly Ile Asn Asn Asn Met Val His Pro Pro Tyr Ile Asn Ser His
 115 120 125
 ggc ttt gga atg ttt gat ttt gac cca tca tgc caa ggg ttt tac agg 432
 Gly Phe Gly Met Phe Asp Phe Asp Pro Ser Ser Gln Gly Phe Tyr Arg
 130 135 140
 gac gat cat aac gct gct tct gga tct ggt ggt ttt gtt gcg cct ttt 480
 Asp Asp His Asn Ala Ala Ser Gly Ser Gly Gly Phe Val Ala Pro Phe
 145 150 155 160
 gat cct tat gct aac atc aaa cgt gat gcc ctg tgatcatgta agaacaacaa 533
 Asp Pro Tyr Ala Asn Ile Lys Arg Asp Ala Leu
 165 170
 ctagtgcattg ctgctttttc acttggttag ttatatccaa gcacaagcac atgcagggtgc 593
 agctgcaact atttagcttc atctacaaat cttttttcct ctcttcttct catgcttttaa 653
 ttatttagag acaataactg ttattcattg ttatgctcaa ttgctagctt ctattcatcg 713
 tcgactgtct gtattgttga tgttcattac agtaacagat aagatggtaa ctgctttact 773
 acttcaaaaa aaaaaaaaaaaa aaa 796

<210> 20

<211> 171
 <212> PRT
 <213> Glycine max

<400> 20
 Ala Arg Ala Met Ala Gly Val Arg Glu Gln Asp Gln Tyr Met Pro Ile
 1 5 10 15
 Ala Asn Val Ile Arg Ile Met Arg Arg Ile Leu Pro Ala His Ala Lys
 20 25 30
 Ile Ser Asp Asp Ala Lys Glu Thr Ile Gln Glu Cys Val Ser Glu Tyr
 35 40 45
 Ile Ser Phe Ile Thr Ala Glu Ala Asn Glu Arg Cys Gln Arg Glu Gln
 50 55 60
 Arg Lys Thr Val Thr Ala Glu Asp Val Leu Trp Ala Met Glu Lys Leu
 65 70 75 80
 Gly Phe Asp Asn Tyr Ala His Pro Leu Ser Leu Tyr Leu His Arg Tyr
 85 90 95
 Arg Glu Ser Glu Gly Glu Pro Ala Ser Val Arg Arg Ala Ser Ser Ala
 100 105 110
 Met Gly Ile Asn Asn Asn Met Val His Pro Pro Tyr Ile Asn Ser His
 115 120 125
 Gly Phe Gly Met Phe Asp Phe Asp Pro Ser Ser Gln Gly Phe Tyr Arg
 130 135 140
 Asp Asp His Asn Ala Ala Ser Gly Ser Gly Gly Phe Val Ala Pro Phe
 145 150 155 160
 Asp Pro Tyr Ala Asn Ile Lys Arg Asp Ala Leu
 165 170

<210> 21
 <211> 1098
 <212> DNA
 <213> Triticum aestivum

<220>
 <221> CDS
 <222> (55)...(894)

<400> 21
 gcacgagcaa gtgcgagtgc gactacctgc attgcacctt ggctagccct agac atg 57
 Met
 1
 gag aac gac ggc gtc ccc aac gga cca gcg gcg ccg gca cct acc cag 105
 Glu Asn Asp Gly Val Pro Asn Gly Pro Ala Ala Pro Ala Pro Thr Gln
 5 10 15
 ggg acg ccg gtg gtg cgg gag cag gac cgg ctg atg ccg atc gcg aac 153
 Gly Thr Pro Val Val Arg Glu Gln Asp Arg Leu Met Pro Ile Ala Asn
 20 25 30
 gtg atc cgc atc atg cgc cgt gcg ctg cct gcc cac gcc aag atc tcc 201
 Val Ile Arg Ile Met Arg Arg Ala Leu Pro Ala His Ala Lys Ile Ser
 35 40 45
 gac gac gcc aag gag gcg att cag gaa tgc gtg tcc gag ttc atc agc 249
 Asp Asp Ala Lys Glu Ala Ile Gln Glu Cys Val Ser Glu Phe Ile Ser
 50 55 60 65
 ttc gtc acc ggc gag gcc aac gaa cgg tgc cgc atg cag cac cgc aag 297
 Phe Val Thr Gly Glu Ala Asn Glu Arg Cys Arg Met Gln His Arg Lys
 70 75 80

acc gtc aac gcc gaa gac atc gtg tgg gcc cta aac cgc ctc ggc ttc Thr Val Asn Ala Glu Asp Ile Val Trp Ala Leu Asn Arg Leu Gly Phe 85 90 95	345
gac gac tac gtc gtg ccc ctc agc gtc ttc ctg cac cgc atg cgc gac Asp Asp Tyr Val Val Pro Leu Ser Val Phe Leu His Arg Met Arg Asp 100 105 110	393
ccc gag gcg ggg aca ggt ggt gcc gct gca ggc gac agc cgc gcc gtg Pro Glu Ala Gly Thr Gly Gly Ala Ala Ala Gly Asp Ser Arg Ala Val 115 120 125	441
acg agt gcg cct ccc cgc gcg gcc ccg ccc gtg atc cac gcc gtg ccg Thr Ser Ala Pro Pro Arg Ala Ala Pro Pro Val Ile His Ala Val Pro 130 135 140 145	489
ctg cag gct cag cgc ccg atg tac gcg ccc ccg gct ccg ttg cag gtt Leu Gln Ala Gln Arg Pro Met Tyr Ala Pro Pro Ala Pro Leu Gln Val 150 155 160	537
gag aat cag atg cag cgg cct gtg tac gct ccc ccg gct ccg gtg cag Glu Asn Gln Met Gln Arg Pro Val Tyr Ala Pro Pro Ala Pro Val Gln 165 170 175	585
gtt cag atg cag cgg ggc atc tat ggg ccc ccg gct cca gtg cac ggg Val Gln Met Gln Arg Gly Ile Tyr Gly Pro Arg Ala Pro Val His Gly 180 185 190	633
tac gcc gtc gga atg gcg ccc gtg ccg gcc aac gtc ggc ggg cag tac Tyr Ala Val Gly Met Ala Pro Val Arg Ala Asn Val Gly Gly Gln Tyr 195 200 205	681
cag gtg ttc ggc gga gag ggt gtc atg gcc cag caa tac tac ggg tac Gln Val Phe Gly Gly Glu Gly Val Met Ala Gln Gln Tyr Tyr Gly Tyr 210 215 220 225	729
ggg tac gag gaa gga gcg tac ggc gca ggt agc agc aac gga gga gcc Gly Tyr Glu Glu Gly Ala Tyr Gly Ala Gly Ser Ser Asn Gly Gly Ala 230 235 240	777
gcc att ggc gac gag gag agc tcg tcc aac ggc gtg ccg gca ccg ggg Ala Ile Gly Asp Glu Glu Ser Ser Ser Asn Gly Val Pro Ala Pro Gly 245 250 255	825
gag ggc atg ggg gag cca gag cca gag cca gca gca gaa gaa tcg cat Glu Gly Met Gly Glu Pro Glu Pro Glu Pro Ala Ala Glu Glu Ser His 260 265 270	873
gac aag ccc gtc caa tct ggc tagtcgcgtg cgcggcgcgc gttagcttct Asp Lys Pro Val Gln Ser Gly 275 280	924
gcgtcctgtg tactgtaata atttgccgtg tcgatccggc catggtttgt gtgtgcgtag tgcttatcta atgtgggctt gtcctctagt aattcatgta ttgcttatct aatgtggact tgtcctctag taattcatgt actctttgct gttgaaaaaa aaaaaaaaaa aaaa	984 1044 1098

<210> 22

<211> 280

<212> PRT

<213> Triticum aestivum

<400> 22

Met Glu Asn Asp Gly Val Pro Asn Gly Pro Ala Ala Pro Ala Pro Thr
 1 5 10 15
 Gln Gly Thr Pro Val Val Arg Glu Gln Asp Arg Leu Met Pro Ile Ala
 20 25 30
 Asn Val Ile Arg Ile Met Arg Arg Ala Leu Pro Ala His Ala Lys Ile
 35 40 45
 Ser Asp Asp Ala Lys Glu Ala Ile Gln Glu Cys Val Ser Glu Phe Ile
 50 55 60
 Ser Phe Val Thr Gly Glu Ala Asn Glu Arg Cys Arg Met Gln His Arg
 65 70 75 80
 Lys Thr Val Asn Ala Glu Asp Ile Val Trp Ala Leu Asn Arg Leu Gly
 85 90 95
 Phe Asp Asp Tyr Val Val Pro Leu Ser Val Phe Leu His Arg Met Arg
 100 105 110
 Asp Pro Glu Ala Gly Thr Gly Gly Ala Ala Ala Gly Asp Ser Arg Ala
 115 120 125
 Val Thr Ser Ala Pro Pro Arg Ala Ala Pro Pro Val Ile His Ala Val
 130 135 140
 Pro Leu Gln Ala Gln Arg Pro Met Tyr Ala Pro Pro Ala Pro Leu Gln
 145 150 155 160
 Val Glu Asn Gln Met Gln Arg Pro Val Tyr Ala Pro Pro Ala Pro Val
 165 170 175
 Gln Val Gln Met Gln Arg Gly Ile Tyr Gly Pro Arg Ala Pro Val His
 180 185 190
 Gly Tyr Ala Val Gly Met Ala Pro Val Arg Ala Asn Val Gly Gly Gln
 195 200 205
 Tyr Gln Val Phe Gly Gly Glu Gly Val Met Ala Gln Gln Tyr Tyr Gly
 210 215 220
 Tyr Gly Tyr Glu Glu Gly Ala Tyr Gly Ala Gly Ser Ser Asn Gly Gly
 225 230 235 240
 Ala Ala Ile Gly Asp Glu Glu Ser Ser Ser Asn Gly Val Pro Ala Pro
 245 250 255
 Gly Glu Gly Met Gly Glu Pro Glu Pro Glu Pro Ala Ala Glu Glu Ser
 260 265 270
 His Asp Lys Pro Val Gln Ser Gly
 275 280

<210> 23
 <211> 65
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> LEC1 consensus protein sequence

<221> VARIANT
 <222> (1)...(65)
 <223> Xaa = Any Amino Acid

<400> 23
 Arg Glu Gln Asp Xaa Xaa Met Pro Ile Ala Asn Val Ile Arg Ile Met
 1 5 10 15
 Arg Xaa Xaa Leu Pro Xaa His Ala Lys Ile Ser Asp Asp Ala Lys Glu
 20 25 30
 Xaa Ile Gln Glu Cys Val Ser Glu Tyr Ile Ser Phe Xaa Thr Xaa Glu
 35 40 45
 Ala Asn Xaa Arg Cys Xaa Xaa Xaa Xaa Arg Lys Thr Xaa Xaa Xaa Glu
 50 55 60
 Xaa
 65